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	MGAGGGWWQVS-PSKKSEIDTIKKVPCETPPFTVGBLKKAIPPHCFKRSIPRSPSYLIWDIIIASCFYYVATTYFPLLPHPLSYFANPLYWACGGCVLTGV
SEQIDNO12 SEQIDNO16	MGAGGRMQVSPPSKKSETDNIKRVPCETPPFTVGBLKKAIPPHCFKRSIPRSFSYLIWDIIIASCFYYVATTYFPLLPHPLSYFANFLYWACQGCVLTGV 100 MGAGGRMQVSPPSKKSETDTIKRVPCETPPFTVGBLKKAIPPHCFKRSIPRSFSYLIWDIIIASCFYYVATTYFPLLPHPLSYFANFLYWACQGCVLTGV 100
	WIAHECGHHAFSDYQWLDDTVGLIFHSPLLVXYFSWKYSHRRHHSNTGSLERDEVFVPKKKSDIKWYGKYLNNPLGRTVMLTVQFTLGNPLYLAFNVSG
	110 120 130 140 150 160 170 180 190 200
SRQIDNO12 SRQIDNO16	WVIAHKCGHHAFSDYQWLDDTVGLIFHSFLLVXYFSWKYSHRRHHSNTGSLERDEVFVPKKKSDIKNYGKYLNNPLGRTVMLTVQFTLGWPLYLAFNVSG 200 WVIAHECGHHAFSDYQWLDDTVGLIFHSFLLVPYFSWKYSHRRHHSNTGSLERDEVFVPKKKSDIKWYGKYHNNPLGRTVMLTVQFTLGWPLYLAFNVSG 200
	RPYDGGFACHFHPNAPIYNDRERLQIYISDAGILAVCYGLFRYAAXQGVASMVCFYGVPLLXVNGFLUTYLQHTHPSLPHYDSSEWDWLRGALATVDR
SEQIDNO12 SEQIDNO16	RPYDGGFACHFHPNAPIYNDRERLQIYISDAGILAVCYGLYRYAAXQGVASNVCFYGVPLLXVNGFLVLITYLQHTHPSLPHYDSSEWDWLRGALATVDR 300 RPYDGGFACHFHPNAPIYNDRERLQIYISDAGILAVCYGLFRYAAAQGVASNVCFYGVPLLIVNGFLVLITYLQHTHPSLPHYDSSEWDWLRGALATVDR 300
	DYGILMKVFHNITDTHVAHHLFSTMPHYHAMBATKAIKPILGBYYQFDGTPVVKAMWREAKBCIYVEPDRQGEKKGVFWYNNKL 310 320 330 340 350 360 370 380
SEQIDNO12 SEQIEMO16	DYGILNKVPHNITDIHVAHHLFSTMPHYHAMBATKAIKPILGBYYQFDGTPVVKAMWRBAKRCIYVBPDRQGBKKGVFWYNNKD DYGILMKYTFINITDIHVAHHLFSTMFHIHIBATKAIKFILGBIYOFDGTFVVKAMWRBAKRCIYVBPDROGEKKGVFWYNNKT.